MULTI-SCALE DIFFEOMORPHIC CORTICAL REGISTRATION UNDER MANIFOLD SULCAL CONSTRAINTS

G. Auzias[1,2], J.-A. Glaunès[3], A. Cachia[2,4], P. Cathier[2,5], E. Bardinet[1,2], O. Colliot[1,2]
J.-F. Mangin[2,5], A. Trouvé[6], S. Baillet[1,2]

[1] Cognitive Neuroscience & Brain Imaging Laboratory, CNRS;
UPMC Univ Paris 6; Hôpital de la Salpêtrière, Paris, France
[2]Federative Institute for Neuroimaging, IFR49, Orsay, France
[3]MAP5, Université Paris 5 - René Descartes, Paris, France
[4]Research Unit of Neuroimaging & Psychiatry,Inserm-CEA, Orsay, France
[5]NeuroSpin, CEA, Orsay, France
[6]CMLA, ENS de Cachan, France

ABSTRACT

Neuroimaging at the group level requires spatial normalization across individuals. This issue has been receiving considerable attention from multiple research groups. Here we suggest a surface-based geometric approach that consists in matching a set of cortical surfaces through their sulcal imprints. We provide the proof-of-concept of this approach by showing 1) how sulci may be automatically identified and simplified from T1-weighted MRI data series, and 2) how this sulcal information may be considered as landmarks for recent measure-based diffeomorphic deformation approaches. In our framework, the resulting 3D transforms are naturally applied to the entire cortical surface and MRI volumes.

Index Terms— MRI, sulcus, diffeomorphisms, volume and surface registration.

1. INTRODUCTION

The problem of inter-individual brain co-registration has already been approached through a considerable number of techniques. Because of substantial variability of the brain in shape and size across individuals, this problem may still be considered as ill-posed and the specific objectives of registration have many faces: e.g., from better detection of functional activations to elaboration of robust indices for emerging applications of computational neuroanatomy. Some groups have recently suggested considering brain co-registration as a surface-matching problem based on geometric features of the cortical manifold such as sulcal shapes [3, 8]. Effectiveness of geometric matching is questioned by 1) the robust and automatic extraction of cortical landmarks and 2) how a surface-based transform would extend to the entire brain volume. We address this issue by using numerous sulcal elements and measure-based diffeomorphisms as we shall now

detail.

2. MATERIAL AND METHODS

Briefly, the automatic extraction from T1-weighted MR images and labelling of a large number of sulci was obtained from the brainVISA free software platform [1, 7]. An automatic simplification procedure of each resulting sulcal ribbon is then applied before the respective sulcal imprints from two individuals are matched at two different scales under the principle of diffeomorphic measure transports [4, 5, 6].

2.1. Robust landmark extraction

Segmentations of CSF, gray and white matter tissues were obtained from histogram analyses and mathematical morphological techniques applied to the biased-corrected T1-weighted MR images (brainVISA, [1]). Elementary sulcal elements were then segmented and divided into topologically-simple surfaces and organized as a graph structure. Once sulci were extracted, they were automatically labelled according to a predefined 90-sulcus label nomenclature. The recognition process relies on a neural network which labeling decisions consider both intrinsic and relational sulcal information as detailed in [7]. Correct-labelling performances reach 75% on average as agreement between the computer and human experts tend to decline for cortical folds with large interindividual variability, though might reach up to 96% for better-defined folds such as e.g. the central sulcus. Again, all the necessary tools are freely available in brainVISA as illustrated Fig.1. Here, we have considered a simplified nomenclature of 46 sulcal labels to avoid the largest labeling errors in areas of strongest interindividual variability.

This non-parametric extraction of geometrical landmarks yields sulcal objects of complex topology. Such detailed de-

scription of cortical folds however could impede subsequent efficient brain registration across a group of subjects. We have therefore simplified these elemental registration landmarks in the following principled manner.
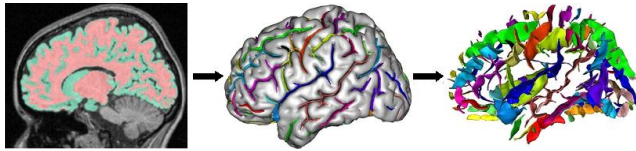

Fig. 1. Segmentation, tessellation and automatic identification of sulci using automated processes from the brainVISA software distribution.

2.2. Robust landmark simplification

The characteristic geometrical features of each sulcus were first reduced to their fundus and outer edges at the cortical level. This is exemplified Fig.2.
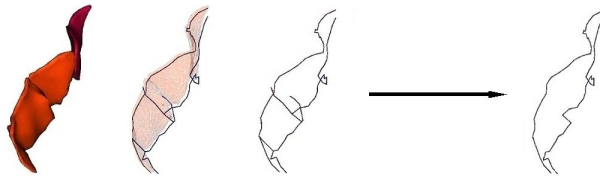

Fig. 2. Sulcal fundus and outer edges of a central sulcus (left, in red) are extracted and simplified. Each sulcus may therefore be summarized by 2 simple but meaningful lines (rightmost view).

Each of these sulcal edges (fundus and outer edge) was individually decomposed into elementary line components by first detecting the singular points of these 3-D discrete curves (i.e end points having only one neighbor and intersection points with more than 2 neighbors) as shown Fig.3(a-c).
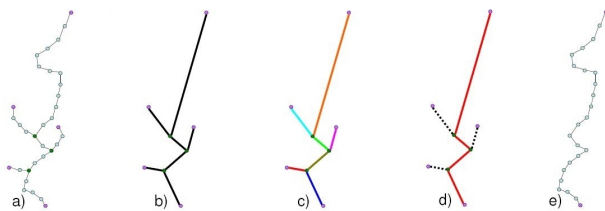

Fig. 3. The original complex sulcal edge illustrated in a) is reduced to a simple line in e) in a principled manner (see text for details).

The secondary branches of the sulcal lines were further identified and removed using a longest-path approach (Fig. 3(d-e)). This topological simplification was applied to every identified sulcus and yielded a uniformly-distributed set of essential folding features across the entire cortical surface – as

shown on rightmost part of Fig. 4. These features hereby define an actual *sulcal fingerprint* that will be matched across individual anatomies.

2.3. Multiscale sulcal registration

Linear co-registration of the two individual brains to be matched was first applied to compensate for the global shape and size differences between subjects. This pre-processing step brings all brains in the standard space of the ICBM152 average template and was achieved using ANIMAL in linear mode [2]. The diffeomorphic transformation now proceeds following the next 3 steps:

1. Clustering of the original 46 sulci in 18 anatomical regional groups: left/right superior temporal, inferior temporal, parietal, occipital, frontal, anterior internal, posterior internal, Sylvian and central areas;

2. Large scale diffeomorphic matching of the resulting ensembles of sulcal elements;

3. Fine scale, pairwise diffeormorphic matching of the entire set of 46 sulcal elements.

The same transformation principles were used for steps 2 and 3 – though with different scaling parameters – which will be detailed in section 2.4.
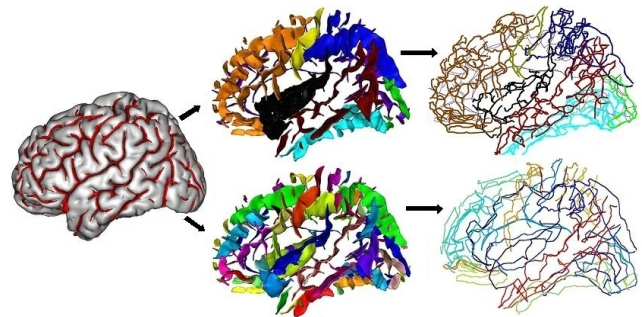

Fig. 4. Two scales of sulcal imprint were extracted from each single brain in the group of individuals to serve as sets of landmarks in the 2-step diffeomorphic matching procedure. Upper row, the large scale, regional nomenclature; bottom row, the finer scale, sulcal nomenclature reveals the detailed sulcal imprint.

2.4. Diffeomorphic matching of sulcus-based measures

The non-linear registration approach is based on recent results on measure-based diffeomorphic transformations which foundations are detailed in [4, 5]. Here each sulcus was considered as a set of points $(x_i)_{i<n_x} \subset \mathbb{R}^3$, which can be described mathematically as a measure μ consisting of a

weighted sum of Dirac distributions:

$$\mu = \sum_{i=1}^{n_x} a_i \delta_{x_i}, \qquad (1)$$

where $(a_i)_{i<n_x}$ is a set of scalar weight parameters. The pairwise diffeomorphic deformation ϕ of sulcus (x_i) onto another sulcus line (y_i) is controlled by integrating time-dependent vector fields $\mathbf{v}_t$ descending from the following flow equation:

$$\partial_t \phi_t = \mathbf{v}_t \circ \phi_t, \quad \phi_0(x) = x, \qquad (2)$$

and $\mathbf{v}_t \in V$, the Hilbert space of regular vector fields, with specific assumptions. In particular, V must be a reproducing kernel Hilbert space with kernel K^v controlling for the regularity of the final diffeomorphic transforms. We define the energy of the deformation as:

$$d_V(\phi, \phi') = \inf \left\{ \int_0^1 ||\mathbf{v}_t||_V^2 dt \mid \in L^2([0,1], V) \; \phi_1^{\mathbf{Y}} \circ \phi = \phi' \right\}$$

The action of ϕ on the measure μ is defined as a mass transportation problem which results in:

$$\phi(\mu) = \phi(\sum_i a_i \delta_{x_i}) = \sum_i a_i \delta_{\phi(x_i)}. \qquad (3)$$

We define μ, the source sulcus to be adjusted to a target sulcal element ν. The pairwise registration of sulcal elements is a measure-matching problem consisting of the minimization in $L^2([0,1], V)$ of the functional:

$$J_{\mu,\nu}^{sulc}(\phi) = \gamma d_V(id, \phi) + ||\phi.\mu - \nu||_{I^*}^2, \qquad (4)$$

where I is another reproducing kernel Hilbert space such that every bounded and signed measure μ and ν belongs to I^*, the dual space of I. The last term in (4) favors the matching of both measures.

Now for two brains with K sulcal labels in common, we define $(\mu^k)_{1 \le k \le K}$ the source sulcal imprint to be adjusted to a target sulcal imprint $(\nu^k)_{1 \le k \le K}$. Pairwise registration of sulcal imprints yields the minimization of a new functional:

$$J_{\mu^k,\nu^k}^{impr}(\phi) = \gamma d_V(id, \phi) + \sum_{k=1}^{K} ||\phi.\mu^k - \nu^k||_{I^*}^2. \qquad (5)$$

The resulting transform is a fully 3D diffeomorphic deformation map defined everywhere in $\mathbb{R}^3$, hence on the cortical surface as illustrated Fig. 5, but also in the entire MRI volume.

2.5. Building a multiple-subject anatomical template

The question of choosing an anatomical template onto which all individual anatomies will eventually be warped is very much dependent on the objective of the registration process. Here, we illustrate how the diffeomorphic transform may be used to construct a sulcal imprint template from all the individual data available according to the following threefold procedure inspired by [6]:
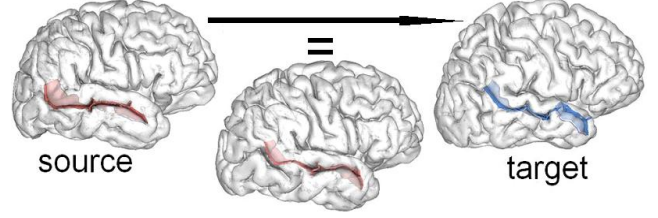

Fig. 5. The superior temporal sulcus (STS) of the source subject (left, in red) is matched to the STS of the target subject (right, in blue). The deformed object is shown at the center. Note how the topology of surrounding structures and surfaces were preserved even though only a single sulcus served as an anatomical landmark to the deformation.

1. Extraction of the individual sulcal information and linear co-registration using ANIMAL in linear mode [2];

2. Diffeomorphic transformation of each individual data to the sample distribution of the entire set of sulcal points at the group level;

3. This process is further iterated Q times by taking the resulting transformed sulcal points as the new target sample for each individual until convergence (small evolution between two successive template samples).

This procedure is applied at the regional and sulcal scales introduced in section 2.3 and therefore yields 2 distinct templates. For clarity purposes and space being limited, we detail the procedure with a single-sulcus template. Generalization to K sulci is a natural extension of Eqs. (4) and (5).

Following [6], we note $(x_{ip})_{1 \le i \le N, 1 \le p \le n_i}$ the N individual point sets of n_i points for which we need to build a template, $a_{ip} \in \mathbb{R}$ their associated weights and $\mu_i = \sum_{p=1}^{n_i} a_{ip} \delta_{x_{ip}}$ their respective measure form. Obtaining the measure μ of the group template may be defined as a minimisation problem:

$$\{\hat{\psi_i}, \hat{\mu}\} = \arg\min_{\psi_i, \mu} \sum_{i=1}^{N} \left\{ \gamma d_V(id, \psi_i) + ||\psi_i \mu_i - \mu||_{I^*}^2 \right\}. \qquad (6)$$

Note that for fixed ψ_i, $\hat{\mu}$ reduces to the sum of the Dirac masses associated to the union of all points $\psi_i(x_{ip})$:

$$\hat{\mu} = \frac{1}{N} \sum_{i=1}^{N} \psi_i \mu_i = \frac{1}{N} \sum_{i=1}^{N} \sum_{p=1}^{n_i} a_{ip} \delta_{\psi_i(x_{ip})}. \qquad (7)$$

Hence, the problem reduces to:

$$\{\hat{\psi_i}\} = \arg\min_{\psi_i} \sum_{i=1}^{N} \left\{ \gamma d_V(id, \psi_i) + ||\psi_i \mu_i - \frac{1}{N} \sum_{i=1}^{N} \psi_i \mu_i||_{I^*}^2 \right\}.$$

Therefore, optimization for solving Eq. (6) consists in Q iterations of N minimization steps with respect to ψ_i with $\psi_j, j \ne i$ fixed and template updating through Eq. (7).

3. RESULTS

We applied this method to the co-registration of 7 subjects to the corresponding group template detailed in section 2.5. 5 iterations consisting of 7 minimization steps were necessary to yield the group template both at the regional and sulcal scales. Fig. 6 illustrates how the superimposition of most sulcal elements clearly improved after diffeomorphic transformation. Further, note that *matching is not warping* as some original features due to intrinsic individual variability have been preserved by the regularity of the transforms.
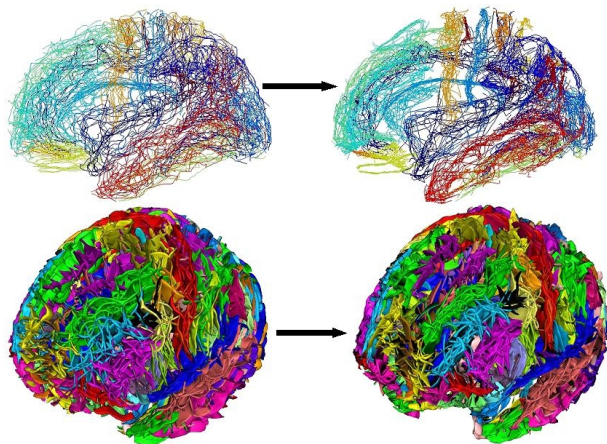

Fig. 6. Comparing linear brain coregistration (left column) and diffeomorphic sulcal matching (right column). Upper row: corresponding sample sulcal imprints; lower row: ribbons representing sulci as surface elements (superio-frontal view). Note how sulcal alignment has improved, e.g. in prefrontal areas.

More quantitatively, the average Hausdorff distance between each subject and the rest of the group was computed for each sulcal landmark. This measure is an indicator of the spatial dispersion of cortical folds, as detailed in the following table (all measures in mm). The largest residual distances were obtained in regions of largest interindividual variability of greater geometrical complexity as in e.g. the occipital lobe, thereby also illustrating the regularity of the resulting transform. Note also that the deformation of any sulcus is also limited by the influence from the sulcal matching in its neighborhood.

4. DISCUSSION

The suggested approach combines the attractive properties of diffeormorphic matching with the usage of geometrical landmarks which are crucial to neuroanatomists. Preliminary results suggest this technique may lead to a new systematic approach for anatomical registration in neuroimaging and computational neuroanatomy group studies.

sulcus	before	after	difference
Superior Post-Central Sulcus	20.6	5.7	14.8
Collateral Fissure	28.1	15.8	12.3
Intraparietal Fissure	27.8	19.2	8.5
Inferior Frontal Sulcus	19.4	11.5	7.8
Calcarine Fissure	17.5	10.3	7.2
Insula	21.0	14.8	6.1
Superior Temporal sulcus	26.1	21.3	4.7
Superior Frontal Sulcus	17.7	13.5	4.1
Pre-Central Sulcus	18.0	16.1	1.9
Occipital	26.1	25.0	1.1
Central Sulcus	15.3	14.7	0.5
average	21.0	14.0	7.0

Table 1. Average Hausdorff distance between each subject and the rest of the group for major sulci, before and after the diffeomorphic registration. All measures are in mm.

5. REFERENCES

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